1 GAP-1 CODING SEQUENCE — SEQ ID NO: 38 and 39

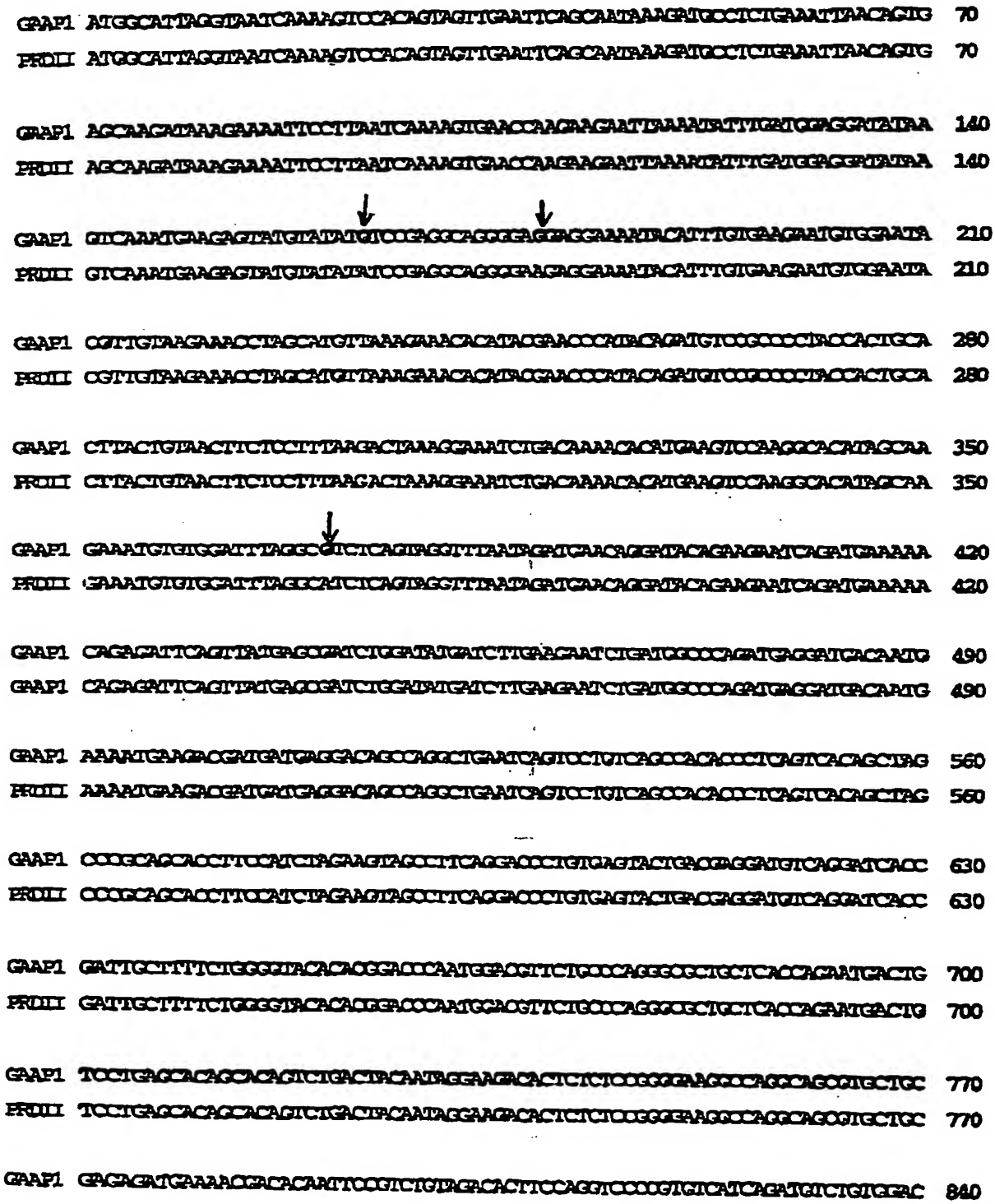

FIGURE 14A (a)

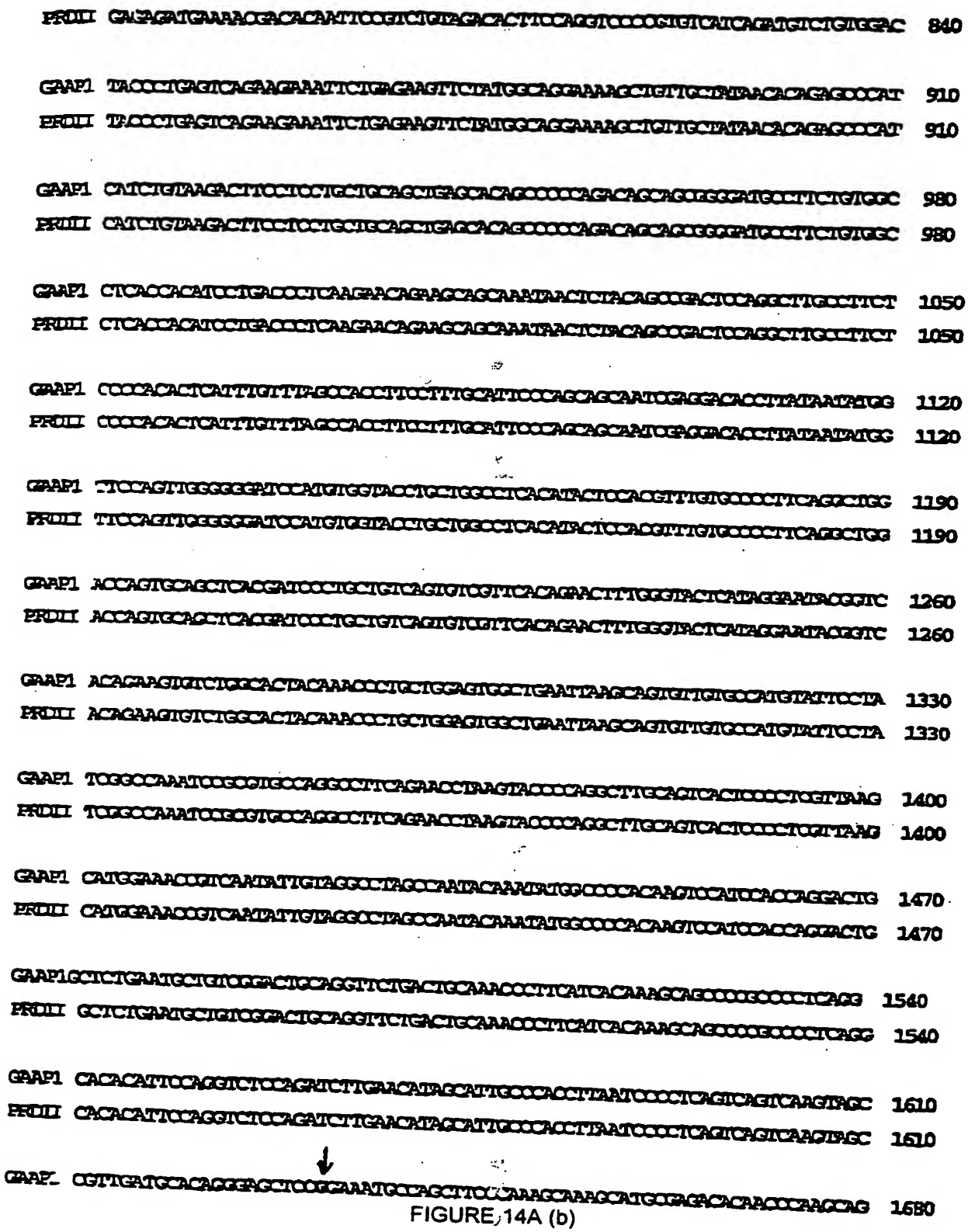
PRDII GAAGAGATGAAAAGACACAATTCCGTCTGTAGACACTTCCAGGTCCCCGTGTCATCAGATGTCTGTGGAC 840
GAAP1 TACCCTGAGTCAGAAGAAATTCTGAGAAGTTCTATGGCAGGAAAAGCTGTTGCTATAACACAGAGCCCAT 910
PRDII TACCCTGAGTCAGAAGAAATTCTGAGAAGTTCTATGGCAGGAAAAGCTGTTGCTATAACACAGAGCCCAT 910
GAAP1 CATCTGTAAGACTTCCTCCTGCTGCAGCTGAGCACAGCCCCAGACAGCAGCAGGGGATGCCTTCTGTGGC 980
PRDII CATCTGTAAGACTTCCTCCTGCTGCAGCTGAGCACAGCCCCAGACAGCAGCAGGGGATGCCTTCTGTGGC 980
GAAP1 CTCACCACATCCTGACCCTCAAGAACAGAAGCAGCAAATAACTCTACAGCCGACTCCAGGCTTGCCTTCT 1050
PRDII CTCACCACATCCTGACCCTCAAGAACAGAAGCAGCAAATAACTCTACAGCCGACTCCAGGCTTGCCTTCT 1050
GAAP1 CCCCACACTCATTTGTTTAGCCACCTTCCTTTGCATTCCCAGCAGCAATCGAGGACACCTTATAATATGG 1120
PRDII CCCCACACTCATTTGTTTAGCCACCTTCCTTTGCATTCCCAGCAGCAATCGAGGACACCTTATAATATGG 1120
GAAP1 CTCCAGTTGGGGGGATCCATGTGGTACCTGCTGGCCTCACATACTCCACGTTTGTGCCCCTTCAGGCTGG 1190
PRDII TTCCAGTTGGGGGGATCCATGTGGTACCTGCTGGCCTCACATACTCCACGTTTGTGCCCCTTCAGGCTGG 1190
GAAP1 ACCAGTGCAGCTCACGATCCCTGCTGTCAGTGTCGTTCACAGAACTTTGGGTACTCATAGGAATACGGTC 1260
PRDII ACCAGTGCAGCTCACGATCCCTGCTGTCAGTGTCGTTCACAGAACTTTGGGTACTCATAGGAATACGGTC 1260
GAAP1 ACAGAAGTGTCTGGCACTACAAACCCTGCTGGAGTGGCTGAATTAAGCAGTGTTGTGCCATGTATTCCTA 1330
PRDII ACAGAAGTGTCTGGCACTACAAACCCTGCTGGAGTGGCTGAATTAAGCAGTGTTGTGCCATGTATTCCTA 1330
GAAP1 TCGGCCAAATCCGCGTGCCAGGCCTCAGAACCTAAGTACCCCAGGCTTGCAGTCACTCCCCTCGTTAAG 1400
PRDII TCGGCCAAATCCGCGTGCCAGGCCTCAGAACCTAAGTACCCCAGGCTTGCAGTCACTCCCCTCGTTAAG 1400
GAAP1 CATGGAAACGGTCAATATTGTAGGCCTAGCCAATACAAATATGGCCCCACAAGTCCATCCACCAGGACTG 1470
PRDII CATGGAAACGGTCAATATTGTAGGCCTAGCCAATACAAATATGGCCCCACAAGTCCATCCACCAGGACTG 1470
GAAP1GCTCTGAATGCTGTCGGACTGCAGGTTCTGACTGCAAACCCTTCATCACAAAGCAGCCCCGCCCTCAGG 1540
PRDII GCTCTGAATGCTGTCGGACTGCAGGTTCTGACTGCAAACCCTTCATCACAAAGCAGCCCCGCCCTCAGG 1540
GAAP1 CACACATTCCAGGTCTCCAGATCTTGAACATAGCATTGCCCACCTTAATCCCCTCAGTCAGTCAAGTAGC 1610
PRDII CACACATTCCAGGTCTCCAGATCTTGAACATAGCATTGCCCACCTTAATCCCCTCAGTCAGTCAAGTAGC 1610
GAAP_ CGTTGATGCACAGGAGCTCCGGAAATGCCAGCTTCCCAAAGCAAGCATGCGAGACACAACCCAAGCAG 1680

FIGURE 14A (b)

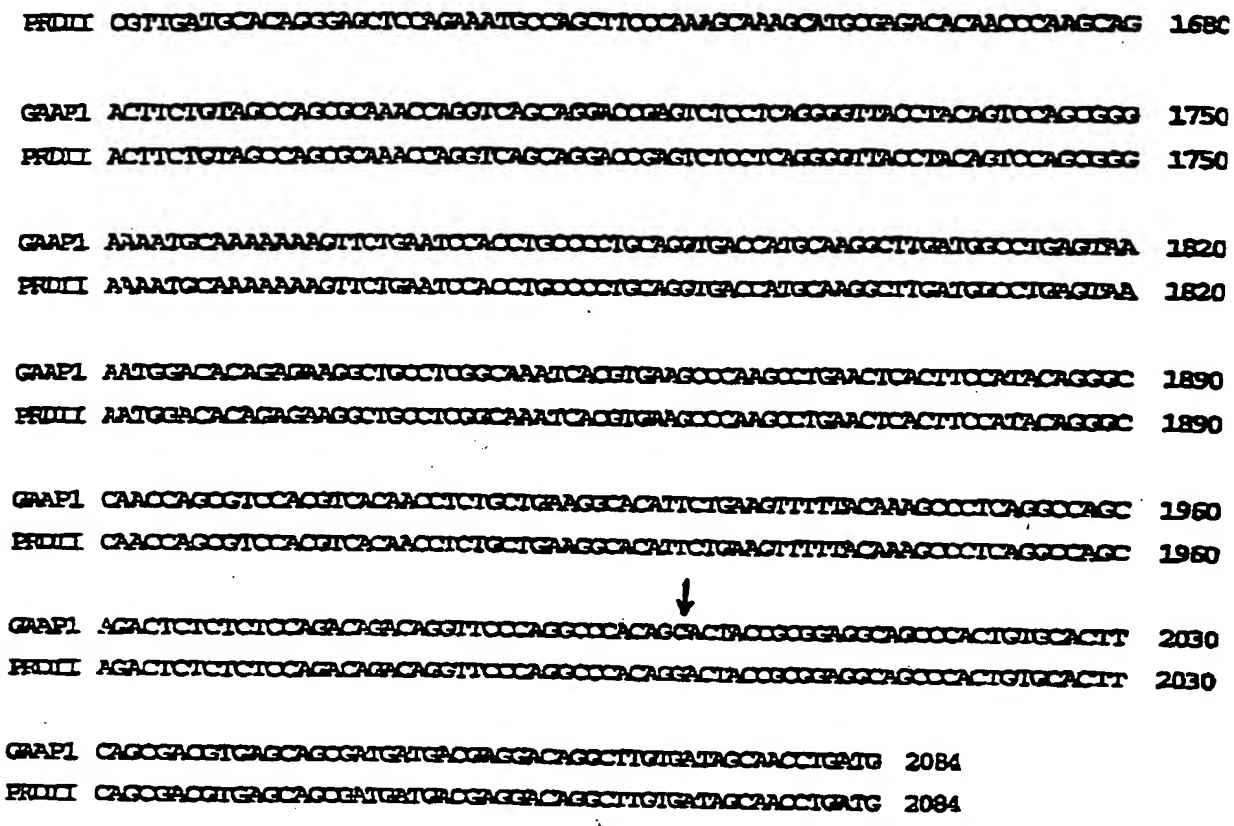
PRDII CGTTGATGCACAGGAGCTCCAGAAATGCCAGCTTCCCAAGCAAAGCATGCGAGACACAACCCAAGCAG 1680
GAAP1 ACTTCTGTAGCCAGCGCAAACCAGGTCAGCAGGACCGAGTCTCCTCAGGGTTACCTACAGTCCAGCGGG 1750
PRDII ACTTCTGTAGCCAGCGCAAACCAGGTCAGCAGGACCGAGTCTCCTCAGGGTTACCTACAGTCCAGCGGG 1750
GAAP1 AAAATGCAAAAAAAGTTCTGAATCCACCTGCCCCTGCAGGTGACCATGCAAGGCTTGATGGCCTGAGTAA 1820
PRDII AAAATGCAAAAAAAGTTCTGAATCCACCTGCCCCTGCAGGTGACCATGCAAGGCTTGATGGCCTGAGTAA 1820
GAAP1 AATGGACACAGAGAAGGCTGCCTGGCAAATCAGGTGAAGCCCAAGCCTGAACTCACTTCCATACAGGGC 1890
PRDII AATGGACACAGAGAAGGCTGCCTGGCAAATCAGGTGAAGCCCAAGCCTGAACTCACTTCCATACAGGGC 1890
GAAP1 CAACCAGCGTCCAGGTCACAACCTCTGCTGAAGGCACATTCTGAAGTTTTTACAAAGCCCTCAGGCCAGC 1960
PRDII CAACCAGCGTCCAGGTCACAACCTCTGCTGAAGGCACATTCTGAAGTTTTTACAAAGCCCTCAGGCCAGC 1960
GAAP1 AGACTCTCTCTCCAGACAGACAGGTTCCCAGGCCCACAGCACTACCGCGAGGCAGCCCACTGTGCACTT 2030
PRDII AGACTCTCTCTCCAGACAGACAGGTTCCCAGGCCCACAGCACTACCGCGAGGCAGCCCACTGTGCACTT 2030
GAAP1 CAGCGACGTGAGCAGCGATGATGACGAGGACAGGCTTGTGATAGCAACCTGATG 2084
PRDII CAGCGACGTGAGCAGCGATGATGACGAGGACAGGCTTGTGATAGCAACCTGATG 2084

FIGURE 14A (c)

1 GAAP-1 CODING SEQUENCE

SEQ ID NO: 44

ATGGGGCAGAAGTTTCAAAAAAAGAGA

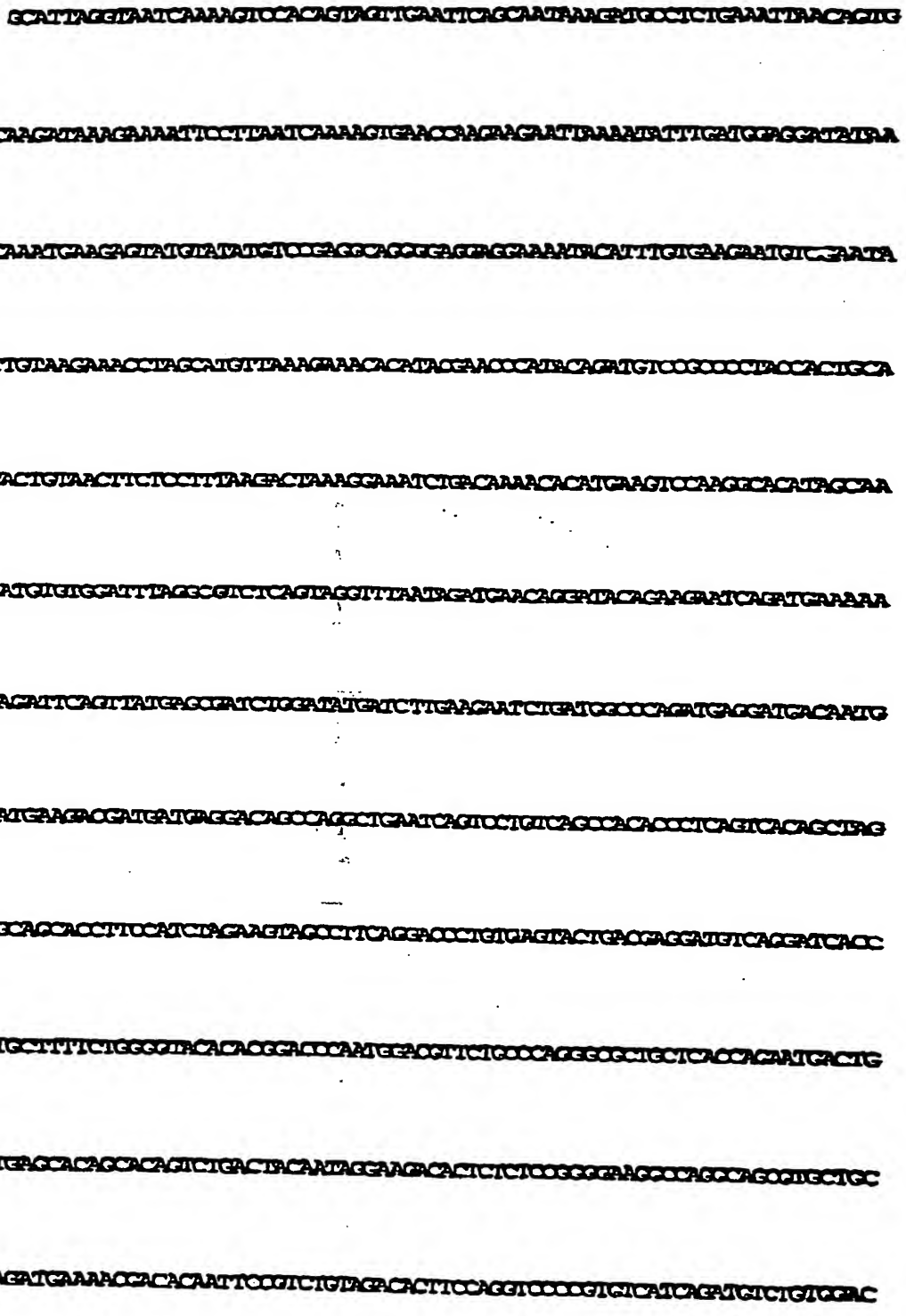

FIGURE 14B (a)

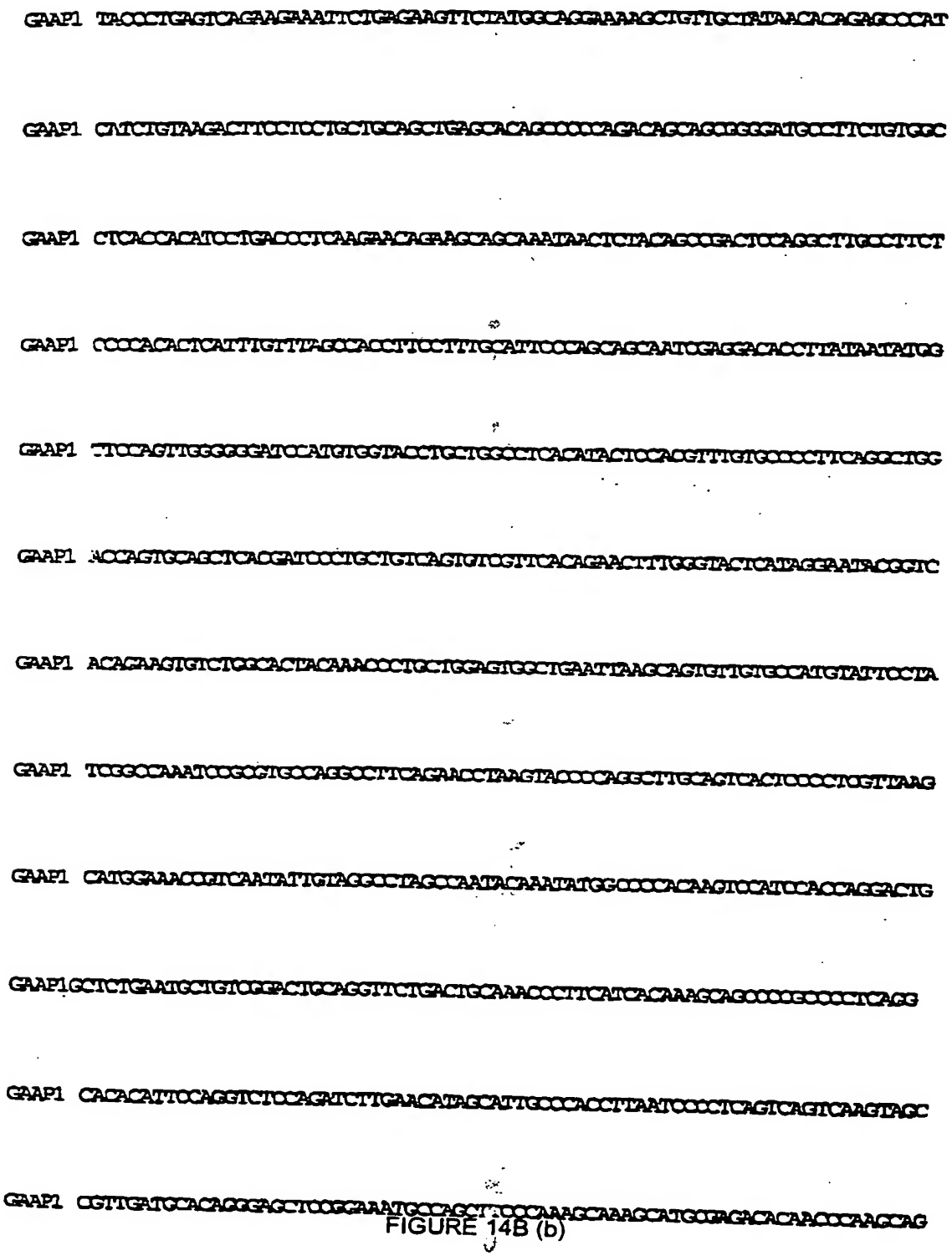

FIGURE 14B (b)

PRDII CGTTGATGCACAGGGAGCTCCAGAAATGCCAGCTTCCCAAAGCAAAGCATGCGAGACACAACCCAAGCAG

GAAP1 ACTTCTGTAGCCAGCGCAAACCAGGTCAGCAGGACCAGTCTCCTCAGGGGTTACCTACAGTCCAGCGGG

GAAP1 AAAATGCAAAAAAAGTTCTGAATCCACCTGCCCCTGCAGGTGACCATGCAAGGCTTGATGGCCTGAGTAA

GAAP1 AATGGACACAGAGAAGGCTGCCTGGCAAATCACGTGAGCCCAAGCCTGAACTCACTTCCATACAGGGC

GAAP1 CAACCAGCGTCCACGTCACAACCTCTGCTGAAGGCACATTCTGAAGTTTTTACAAAGCCCTCAGGCCAGC

GAAP1 AGACTCTCTCTCCAGACAGACAGGTTCCCAGGCCCACAGCACTACCGCGGAGGCAGCCCACTGTGCACTT

GAAP1 CAGCGACGTCAGCAGCGATGATGACGAGGACAGGCTTGTGATAGCAACCTGATG

FIGURE 14B (c)

GAAP-2 coding seq 22/28 SEQ ID NO: 45

```
   1  ATGGGGCAGA AGTTTCAAAA AAAGAAATCT TACAGGCTGG TGTTAAAGGA
      TACCCCGTCT TCAAAGTTTT TTTCTTTAGA ATGTCCGACC ACAATTTCCT

  51  ACTTCGGAAT CCCTTAAAGA GAGCATTAGG TAATCAAAAG TCCACAGTAG
      TGAAGCCTTA GGGAATTTCT CTCGTAATCC ATTAGTTTTC AGGTGTCATC

 101  TTGAATTCAG CAATAAAGAT GCCTCTGAAA TTAACAGTCA GCAAGATAAA
      AACTTAAGTC GTTATTTCTA CGGAGACTTT AATTGTCACT CGTTCTATTT

 151  GAAAATTCCT TAATCAAAAG TGAACCAAGA AGAATTAAAA TATTTGATGG
      CTTTTAAGGA ATTAGTTTTC ACTTGGTTCT TCTTAATTTT ATAAACTACC

 201  AGGATATAAG TCAAATGAAG AGTATGTATA TATCCGAGGC AGGGGAAGAG
      TCCTATATTC AGTTTACTTC TCATACATAT ATAGGCTCCG TCCCCTTCTC

 251  GAAAATACAT TTGTGAAGAA TGTGGAATAC GTTGTAAGAA ACCTAGCATG
      CTTTTATGTA AACACTTCTT ACACCTTATG CAACATTCTT TGGATCGTAC

 301  TTAAAGAAAC ACATACGAAC CCATACAGAT GTCCGCCCCT ACCACTGCAC
      AATTTCTTTG TGTATGCTTG GGTATGTCTA CAGGCGGGGA TGGTGACGTG

 351  TTACTGTAAC TTCTCCTTTA AGACTAAAGG AAATCTGACA AAACACATGA
      AATGACATTG AAGAGGAAAT TCTGATTTCC TTTAGACTGT TTTGTGTACT

 401  AGTCCAAGGC ACATAGCAAG AAATGTGTGG ATTTAGGCAT CTCAGTAGGT
      TCAGGTTCCG TGTATCGTTC TTTACACACC TAAATCCGTA GAGTCATCCA

 451  TTAATAGATG AACAGGATAC AGAAGAATCA GATGAAAAAC AGAGATTCAG
      AATTATCTAC TTGTCCTATG TCTTCTTAGT CTACTTTTTG TCTCTAAGTC

 501  TTATGAGCGA TCTGGATATG ATCTTGAAGA ATCTGATGGC CCAGATGAGG
      AATACTCGCT AGACCTATAC TAGAACTTCT TAGACTACCG GGTCTACTCC

 551  ATGACAATGA AAATGAAGAC GATGATGAGG ACAGCCAGGC TGAATCAGTC
      TACTGTTACT TTTACTTCTG CTACTACTCC TGTCGGTCCG ACTTAGTCAG

 601  CTGTCAGCCA CACCCTCAGT CACAGCTAGC CCGCAGCACC TTCCATCTAG
      GACAGTCGGT GTGGGAGTCA GTGTCGATCG GGCGTCGTGG AAGGTAGATC

 651  AAGTAGCCTT CAGGACCCTG TGAGTACTGA CGAGGATGTC AGGATCACCG
      TTCATCGGAA GTCCTGGGAC ACTCATGACT GCTCCTACAG TCCTAGTGGC

 701  ATTGCTTTTC TGGGGTACAC ACGGACCCAA TGGACGTTCT GCCCAGGGCG
      TAACGAAAAG ACCCCATGTG TGCCTGGGTT ACCTGCAAGA CGGGTCCCGC

 751  CTGCTCACCA GAATGACTGT CCTGAGCACA GCACAGTCTG ACTACAATAG
      GACGAGTGGT CTTACTGACA GGACTCGTGT CGTGTCAGAC TGATGTTATC

 801  GAAGACACTC TCTCCGGGGA AGGCCAGGCA GCGTGCTGCG AGAGATGAAA
      CTTCTGTGAG AGAGGCCCCT TCCGGTCCGT CGCACGACGC TCTCTACTTT

 851  ACGACACAAT TCCGTCTGTA GACACTTCCA GGTCCCCGTG TCATCAGATG
      TGCTGTGTTA AGGCAGACAT CTGTGAAGGT CCAGGGGCAC AGTAGTCTAC

 901  TCTGTGGACT ACCCTGAGTC AGAAGAAATT CTGAGAAGTT CTATGGCAGG
      AGACACCTGA TGGGACTCAG TCTTCTTTAA GACTCTTCAA GATACCGTCC
```

FIGURE 14C (a)

```
 951  AAAAGCTGTT GCTATAACAC AGAGCCCATC ATCTGTAAGA CTTCCTCCTG
      TTTTCGACAA CGATATTGTG TCTCGGGTAG TAGACATTCT GAAGGAGGAC
-------------------------------------------------------------------------------
1001  CTGCAGCTGA GCACAGCCCC CAGACAGCAG CGGGGATGCC TTCTGTGGCC
      GACGTCGACT CGTGTCGGGG GTCTGTCGTC GCCCCTACGG AAGACACCGG
-------------------------------------------------------------------------------
1051  TCACCACATC CTGACCCTCA AGAACAGAAG CAGCAAATAA CTCTACAGCC
      AGTGGTGTAG GACTGGGAGT TCTTGTCTTC GTCGTTTATT GAGATGTCGG
-------------------------------------------------------------------------------
1101  GACTCCAGGC TTGCCTTCTC CCCACACTCA TTTGTTTAGC CACCTTCCTT
      CTGAGGTCCG AACGGAAGAG GGGTGTGAGT AAACAAATCG GTGGAAGGAA
-------------------------------------------------------------------------------
1151  TGCATTCCCA GCAGCAATCG AGGACACCTT ATAATATGCT TCCAGTTGGG
      ACGTAAGGGT CGTCGTTAGC TCCTGTGGAA TATTATACGA AGGTCAACCC
-------------------------------------------------------------------------------
1201  GGGATCCATG TGGTACCTGC TGGCCTCACA TACTCCACGT TTGTGCCCCT
      CCCTAGGTAC ACCATGGACG ACCGGAGTGT ATGAGGTGCA AACACGGGGA
-------------------------------------------------------------------------------
1251  TCAGGCTGGA CCAGTGCAGC TCACGATCCC TGCTGTCAGT GTCGTTCACA
      AGTCCGACCT GGTCACGTCG AGTGCTAGGG ACGACAGTCA CAGCAAGTGT
-------------------------------------------------------------------------------
1301  GAACTTTGGG TACTCATAGG AATACGGTCA CAGAAGTGTC TGGCACTACA
      CTTGAAACCC ATGAGTATCC TTATGCCAGT GTCTTCACAG ACCGTGATGT
-------------------------------------------------------------------------------
1351  AACCCTGCTG GAGTGGCTGA ATTAAGCAGT GTTGTGCCAT GTATTCCTAT
      TTGGGACGAC CTCACCGACT TAATTCGTCA CAACACGGTA CATAAGGATA
-------------------------------------------------------------------------------
1401  CGGCCAAATC CGCGTGCCAG GCCTTCAGAA CCTAAGTACC CCAGGCTTGC
      GCCGGTTTAG GCGCACGGTC CGGAAGTCTT GGATTCATGG GGTCCGAACG
-------------------------------------------------------------------------------
1451  AGTCACTCCC CTCGTTAAGC ATGGAAACCG TCAATATTGT AGGCCTAGCC
      TCAGTGAGGG GAGCAATTCG TACCTTTGGC AGTTATAACA TCCGGATCGG
-------------------------------------------------------------------------------
1501  AATACAAATA TGGCCCCACA AGTCCATCCA CCAGGACTGG CTCTGAATGC
      TTATGTTTAT ACCGGGGTGT TCAGGTAGGT GGTCCTGACC GAGACTTACG
-------------------------------------------------------------------------------
1551  TGTCGGACTG CAGGTTCTGA CTGCAAACCC TTCATCACAA AGCAGCCCCG
      ACAGCCTGAC GTCCAAGACT GACGTTTGGG AAGTAGTGTT TCGTCGGGGC
-------------------------------------------------------------------------------
1601  CCCCTCAGGC ACACATTCCA GGTCTCCAGA TCTTGAACAT AGCATTGCCC
      GGGGAGTCCG TGTGTAAGGT CCAGAGGTCT AGAACTTGTA TCGTAACGGG
-------------------------------------------------------------------------------
1651  ACCTTAATCC CCTCAGTCAG TCAAGTAGCC GTTGATGCAC AGGGAGCTCC
      TGGAATTAGG GGAGTCAGTC AGTTCATCGG CAACTACGTG TCCCTCGAGG
-------------------------------------------------------------------------------
1701  AGAAATGCCA GCTTCCCAAA GCAAAGCATG CGAGACACAA CCCAAGCAGA
      TCTTTACGGT CGAAGGGTTT CGTTTCGTAC GCTCTGTGTT GGGTTCGTCT
-------------------------------------------------------------------------------
1751  CTTCTGTAGC CAGCGCAAAC CAGGTCAGCA GGACCGAGTC TCCTCAGGGG
      GAAGACATCG GTCGCGTTTG GTCCAGTCGT CCTGGCTCAG AGGAGTCCCC
-------------------------------------------------------------------------------
1801  TTACCTACAG TCCAGCGGGA AAATGCAAAA AAAGTTCTGA ATCCACCTGC
      AATGGATGTC AGGTCGCCCT TTTACGTTTT TTTCAAGACT TAGGTGGACG
-------------------------------------------------------------------------------
1851  CCCTGCAGGT GACCATGCAA GGCTTGATGG CCTGAGTAAA ATGGACACAG
      GGGACGTCCA CTGGTACGTT CCGAACTACC GGACTCATTT TACCTGTGTC
-------------------------------------------------------------------------------
```

FIGURE 14C (b)

```
1901  AGAAGGCTGC CTCGGCAAAT CACGTGAAGC CCAAGCCTGA ACTCACTTCC
      TCTTCCGACG GAGCCGTTTA GTGCACTTCG GGTTCGGACT TGAGTGAAGG
-------------------------------------------------------------------------
1951  ATACAGGGCC AACCAGCGTC CACGTCACAA CCTCTGCTGA AGGCACATTC
      TATGTCCCGG TTGGTCGCAG GTGCAGTGTT GGAGACGACT TCCGTGTAAG
-------------------------------------------------------------------------
2001  TGAAGTTTTT ACAAAGCCCT CAGGCCAGCA GACTCTCTCT CCAGACAGAC
      ACTTCAAAAA TGTTTCGGGA GTCCGGTCGT CTGAGAGAGA GGTCTGTCTG
-------------------------------------------------------------------------
2051  AGGTTCCCAG GCCCACAGGA CTACCGCGGA GGCAGCCCAC TGTGCACTTC
      TCCAAGGGTC CGGGTGTCCT GATGGCGCCT CCGTCGGGTG ACACGTGAAG
-------------------------------------------------------------------------
2101  AGCGACGTGA GCAGCGATGA TGACGAGGAC AGGCTTGTGA TAGCAACCTG
      TCGCTGCACT CGTCGCTACT ACTGCTCCTG TCCGAACACT ATCGTTGGAC
-------------------------------------------------------------------------
2151  A
      T
-------------------------------------------------------------------------
```

FIGURE 14C (c)

SEQ ID NO: 40 and 41

2 GAAP-1 POLYPEPTIDE

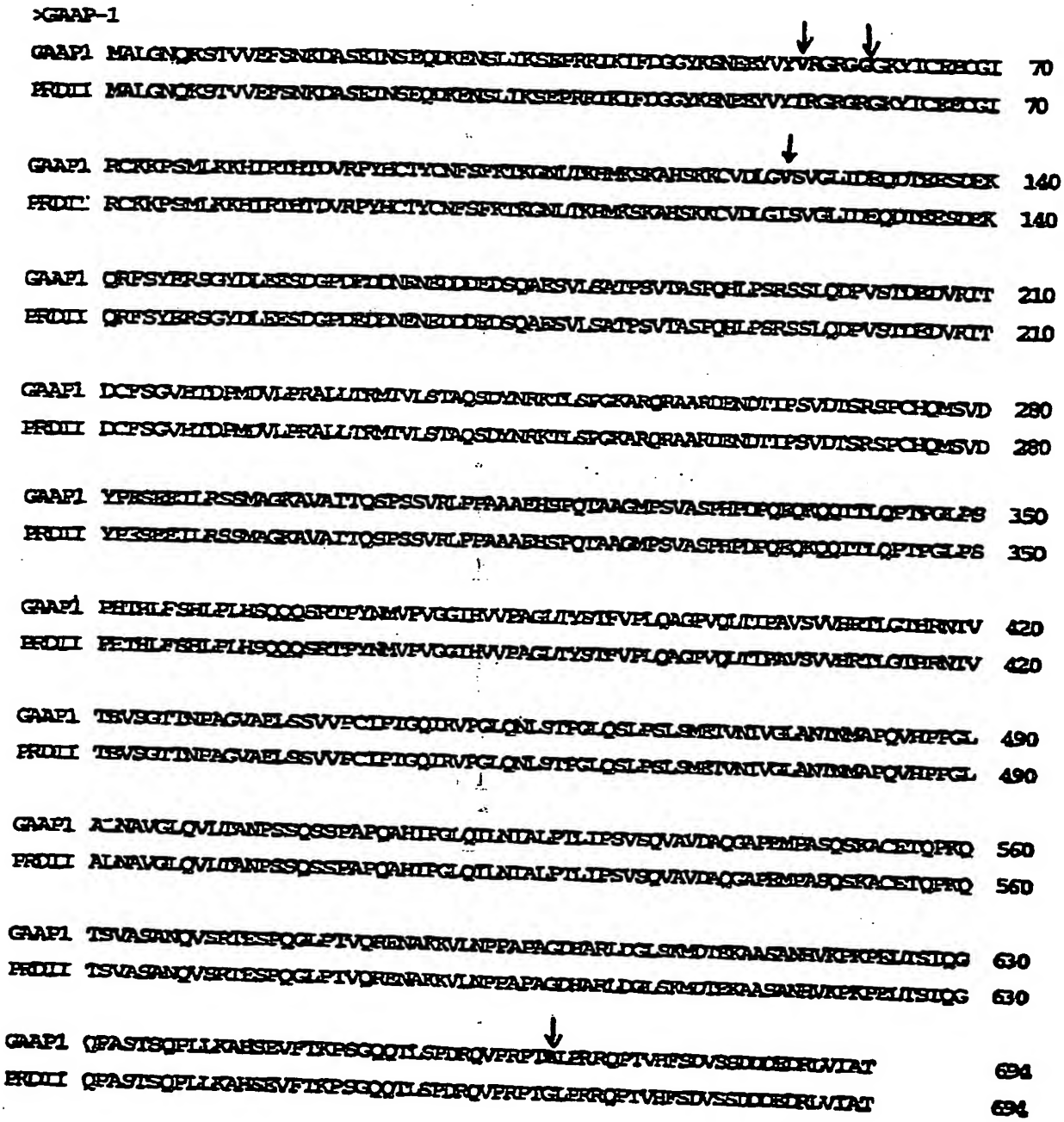

FIGURE 15 A

SEQ ID NO: 46

2 GAAP-1 POLYPEPTIDE

>GAAP-1

M GQKFQKKR. ALGNQKSIVVEFSNKDASKINSEQLKENSLIKSEPRRIKIFDGGYKSNEEYVYVRGGGGKYICEFDGI

GAAP1 RCKKPSMLKKHIRIHTGVRPYHCTYCNFSFKTKGNLIKHMKSKAHSKKCVDLGVSVGLIDEQDTEESDEK

GAAP1 QRFSYERSGYDLSESDGFDEDDNENEDDEDSQAESVLSATPSVIASPQHLPSRSSLQDPVSTDEDVRIT

GAAP1 DCFSGVETDRMDVLPRALLTRMTVLSTAQSDYNRKTLSPGKARQRAARDENDTTPSVDTSRSPCHQMSVD

GAAP1 YPESEELLRSSMAGKAVATTQSPSSVRLPFAAAEHSPQTAAGMPSVASPHPDPQEQKQQTTLQPTPGLPS

GAAP1 PHTHLFSHLPLHSQQQSPTPYNMVPVGGIHVVPAGLTYSTFVPLQAGPVQLTTPAVSVVHPTLGTHRNTV

GAAP1 TEVSGTTNPAGVAELSSVVPCLPTGQIRVPGLQNLSTPGLQSLPSLSMETVNTVGLANTNMAPQVHPPGL

GAAP1 ANAVGLQVLTANPSSQSSPAPQAHTPGLQTLNTALPTLTPSVSQVAVDAQGAPEMPASQSKGCETQPKQ

GAAP1 TSVASANQVSRTESPQGLPTVQRENAKKVLNPPAPAGDHARLDGLSKMDTEKAASANHVKPKPELTSIQG

GAAP1 QPASTSQPLLKAHSEVFTKPSGQQTLSPDRQVPRPTALPRRQPTVHFSDVSSDDDEDRLVTAT

FIGURE 15 B

GAAP-2

SEQ ID NO: 47

```
  1  MGQKFQKKKS YRLVLKELRN PLKRALGNQK STVVEFSNKD ASEINSEQDK
 51  ENSLIKSEPR RIKIFDGGYK SNEEYVYIRG RGRGKYICEE CGIRCKKPSM
101  LKKHIRTHTD VRPYHCTYCN FSFKTKGNLT KHMKSKAHSK KCVDLGISVG
151  LIDEQDTEES DEKQRFSYER SGYDLEESDG PDEDDNENDD DDEDSQAESV
201  LSATPSVTAS PQHLPSRSSL QDPVSTDEDV RITDCFSGVH TDPMDVLPRA
251  LLTRMTVLST AQSDYNRKTL SPGKARQRAA RDENDTIPSV DTSRSPCHQM
301  SVDYPESEEI LRSSMAGKAV AITQSPSSVR LPPAAAEHSP QTAAGMPSVA
351  SPHPDPQEQK QQITLQPTPG LPSPHTHLFS HLPLHSQQQS RTPYNMVPVG
401  GIHVVPAGLT YSTFVPLQAG PVQLTIPAVS VVHRTLGTHR NTVTEVSGTT
451  NPAGVAELSS VVPCIPIGQI RVPGLQNLST PGLQSLPSLS METVNIVGLA
501  NTNMAPQVHP PGLALNAVGL QVLTANPSSQ SSPAPQAHIP GLQILNIALP
551  TLIPSVSQVA VDAQGAPEMP ASQSKACETQ PKQTSVASAN QVSRTESPQG
601  LPTVQRENAK KVLNPPAPAG DHARLDGLSK MDTEKAASAN RVKPKPELTS
651  IQGQPASTSQ PLLKAHSEVF TKPSGQQTLS PDRQVPRPTG LPRRQPTVHF
701  SDVSSDDDED RLVIAT
```

FIGURE 15 C